

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:41:42 ; Search time 54.4414 Seconds  
(without alignments)  
1362.510 Million cell updates/sec

Title: US-09-625-573-4  
Perfect score: 1900  
Sequence: 1 MISTRSRFRINTNESGEV.....DGVSTNTSTGQEVSAAGL 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_21.\*
- 1: sp.archaea.\*
  - 2: sp.bacteria.\*
  - 3: sp.fungi.\*
  - 4: sp.human.\*
  - 5: sp.invertebrate.\*
  - 6: sp.mammal.\*
  - 7: sp.mnc.\*
  - 8: sp.organelle.\*
  - 9: sp.phage.\*
  - 10: sp.plant.\*
  - 11: sp.rodent.\*
  - 12: sp.virus.\*
  - 13: sp.vertebrate.\*
  - 14: sp.unclassified.\*
  - 15: sp.rvirus.\*
  - 16: sp.bacteriaph.\*
  - 17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1392	73.3	352	6	Q95NC2	Q95nc2 callicebus
2	1375	72.4	352	6	Q77776	Q77776 cercopithec
3	1375	72.4	352	6	Q9MZA0	Q9mza0 callithrix
4	1373	72.3	352	6	Q95NE1	Q95ne1 cercopithec
5	1371	72.2	352	6	Q9XT12	Q9xt12 cercopithec
6	1371	72.2	352	6	Q95NC9	Q95nc9 alouatta se
7	1371	72.2	352	6	Q95NC4	Q95nc4 ateles geof
8	1368	72.0	352	6	Q18770	Q18770 pan troglod
9	1368	72.0	352	6	Q9TV49	Q9tv49 cercopithec
10	1367	71.9	352	6	Q9M299	Q9m299 ateles sp.
11	1366	71.9	352	6	Q95ND1	Q95nd1 mandrillus
12	1366	71.9	352	6	Q95NC0	Q95nc0 hylobates m
13	1365	71.8	352	6	Q9XS99	Q9xs99 gorilla gor
14	1365	71.8	352	6	Q95NC5	Q95nc5 hylobates s
15	1364	71.8	352	6	Q95ND2	Q95nd2 mandrillus
16	1364	71.8	352	6	Q95ND0	Q95nd0 erythrocebu

17	1364	71.8	352	6	Q95NC1	Q95nc1 theropithec
18	1364	71.8	352	6	Q97975	Q97975 macaca arct
19	1363	71.7	352	6	Q9TV50	Q9tv50 pan troglod
20	1363	71.7	352	6	Q9TV93	Q9tv93 macaca arct
21	1362	71.7	352	6	Q95NC8	Q95nc8 colobus pol
22	1361	71.6	352	6	Q9XT13	Q9xt13 papio anubi
23	1361	71.6	352	6	Q95NC7	Q95nc7 nasalis lar
24	1360	71.6	352	6	Q9TSK1	Q9tsk1 cercopithec
25	1360	71.6	352	6	Q9TV42	Q9tv42 cercopithec
26	1360	71.6	352	6	Q97962	Q97962 pygathrix a
27	1360	71.6	352	6	Q9XS35	Q9xs35 macaca neme
28	1359	71.5	352	6	Q9TV48	Q9tv48 cercopithec
29	1358	71.5	352	6	Q18771	Q18771 pan troglod
30	1358	71.5	352	6	Q18772	Q18772 pan troglod
31	1358	71.5	352	6	Q9XT14	Q9xt14 colobus gue
32	1358	71.5	352	6	Q95NC3	Q95nc3 miopithecus
33	1357	71.4	339	6	Q9TV08	Q9tv08 saguinus sp
34	1357	71.4	352	6	Q9TV46	Q9tv46 cercopithec
35	1357	71.4	352	6	Q95NE8	Q95ne8 cercopithec
36	1357	71.4	352	6	Q9XT76	Q9xt76 cercopithec
37	1356	71.4	352	6	Q9TV44	Q9tv44 cercopithec
38	1355	71.3	352	6	Q9BGN5	Q9bgn5 cercopithec
39	1354	71.3	352	6	Q9MZA3	Q9mza3 hylobates a
40	1353	71.2	339	6	Q9TSN3	Q9tsn3 macaca fasc
41	1353	71.2	339	6	Q9TQT3	Q9tqt3 callithrix
42	1353	71.2	352	6	Q95NC6	Q95nc6 trachypithe
43	1352	71.2	352	6	Q9TV47	Q9tv47 cercopithec
44	1351	71.1	339	6	Q9TV02	Q9tv02 alouatta ca
45	1351	71.1	352	6	Q9TQX0	Q9tqx0 cercopithec

ALIGNMENTS

RESULT 1

Q95NC2 ID Q95NC2 PRELIMINARY; PRT; 352 AA.  
AC Q95NC2;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.  
OS Callicebus moloch (Dusky titi).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;  
OC Callicebus.  
OX NCBI\_TaxID=9523;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF177887; AAK43370.1; -.  
DR InterPro; IPR000923; BlueCu 1.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN\_1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 73.3%; Score 1392; DB 6; Length 352;  
Best Local Similarity 75.4%; Pred. No. 6.7e-112;  
Matches 263; Conservative 30; Mismatches 50; Indels 6; Gaps 2;

QY 18 EEVTFDYDYG--PCHKFDVKOIGAOQLPPLYSLVIFGFGVGNMLVLLINCKKLKC 75

Db 4 EVSPFIDIDIGASEPQKQIKQWQAOQLPPLYSMLVFGVGNMLVLLINCKRLKS 63

QY 76 LTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGVFGGIFPILIT 135

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Db 64 MTDHYLLNLALSDLEFFLTPFWAHYAAGQWDFGNTMCOFLTGLYFGFFSIFILLT 123
QY 136 IDRYLAIHVAFAKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVVCGPYP 195
Db 124 IDRYLAIHVAFAKARTVTFGVTSVITWVAVFASLPGIIFTRSQEGYHTCSPHP 183
QY 196 RG----WNFHITMRNLGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMV 251
Db 184 FGQYRFWKNLETKMVLGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMV 243
QY 252 YELFWTPYNIIVILLTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEX 311
Db 244 YELFWAPYNIIVILLTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEX 303
QY 312 FRYLSVFRKHITRKQKQCPVFEYRETVDGVTSTNTPTSTGEQEVSA 360
Db 304 FRYLLVFFQKHIAKFKCCSIFQKEAPERANSVYTRSTGEQEVSA 352

RESULT 2
ID 07776 PRELIMINARY; PRT; 352 AA.
AC 07776;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chemokine receptor CCR5.
GN CCR5.
OS Cercopithecus torquatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinæ; Cercocoebus.
OX NCBI_TaxID=81944;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1208;
RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
RA Aguilar R., Ho D.D., Marx P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
RT with a R2b-tropic simian immunodeficiency virus.";
RL J. Exp. Med. 0:0-0(1998).
DR EMBL; AF084004; AAC62472.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473D1D3 CRC64;

Query Match 72.4%; Score 1375; DB 6; Length 352;
Best Local Similarity 76.1%; Pred. No. 1.9e-110;
Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

QY 24 FDYDYG--GAPCHKFDVKIGAQQLPPLYSLSVFIQFVGNMVLVILINCKKLCRTDIYL 81
Db 10 YDIDYSEPCCKIDVKOMGAHLLPPLYSLSVFIQFVGNMVLVILINCKKLCRTDIYL 69
QY 82 LNLALSLLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 141
Db 70 LNLALSLLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTRCKEDSVVVCGPYP----RG 197
Db 130 IVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGYHTCSPHPFQYQF 189
QY 198 WNFHITMRNLGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFW 257
Db 190 WNFETLKLIVLGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFW 249
QY 258 PNYVILLNTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEXKFRYLS 317
Db 250 PNYVILLNTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEXKFRYLS 309

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Db 250 PNYVILLNTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEXKFRYLS 309
QY 318 VFFRKHITKRECKQCPVFEYRETVDGVTSTNTPTSTGEQEVSA 360
Db 310 VFFOKHIAKRECKCSIFQKEASERASSVYTRSTGEQEVSA 352

RESULT 3
ID 09MZA0 PRELIMINARY; PRT; 352 AA.
AC 09MZA0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CC chemokine receptor 5 (C-C chemokine receptor 5).
GN CCR5.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317091; PubMed=10747879;
RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA Begum K., Galvis M.C., Kostecky V., Valente A.J., Murthy K.K.,
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
RT and mRNA. Potential roles for haplotype and mRNA diversity, and altered
RT differential haplotype-specific transcriptional activity, and altered
RT transcription factor binding to polymorphic nucleotides in the
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252554; AAF87984.1; -
DR EMBL; AF177878; AAK43361.1; -
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;

Query Match 72.4%; Score 1375; DB 6; Length 352;
Best Local Similarity 75.2%; Pred. No. 1.9e-110;
Matches 258; Conservative 33; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDYG--APCHKFDVKIGAQQLPPLYSLSVFIQFVGNMVLVILINCKKLCRTDIYL 81
Db 10 YDIDYSEPCCKIDVKOMGAHLLPPLYSLSVFIQFVGNMVLVILINCKKLCRTDIYL 69
QY 82 LNLALSLLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 141
Db 70 LNLALSLLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTRCKEDSVVVCGPYP----RG 197
Db 130 IVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGYHTCSPHPFQYQF 189
QY 198 WNFHITMRNLGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFW 257
Db 190 WNFETLKLIVLGLVPLLMVICYSGLKTLRLCRNEKKRRHRAVRVIFTIMIVYELFW 249
QY 258 PNYVILLNTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEXKFRYLS 317
Db 250 PNYVILLNTFOEFFGLSNCESTSDOQATVETLGMTCCNPIIYAVGEXKFRYLS 309

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR RECEPTOR; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 352 AA; 40420 MW; 3DBB43D1CCA48687 CRC64;

Query Match 72.2%; Score 1371; DB 6; Length 352;
Best Local Similarity 75.2%; Pred. No. 4.3e-110;
Matches 258; Conservative 30; Mismatches 49; Indels 6; Gaps 2;

QY 24 FDYDGA--PCHKFDVKQIGAQLLPPLYSLVYFIFGVGNMVLVLLINCKKLCITDIYL 81
Db 10 YDIDYGASEPCQKTDVQKGAHLLPPLYSIVLFGVGNMVLVLLINCKKPSMTDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISDLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
Db 130 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRRHRAVRVIFTMIVYFLEWT 257
Db 190 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRRHRAVRVIFTMIVYFLEWT 249
QY 258 PYNIVILLNTQFEEFGLSNCESTSDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVILLNTQFEEFGLSNCESTSDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
QY 318 VFFRKHITKRCCKCPVYRETVDGVTSTNTPTSTGEQVSAGL 360
Db 310 VFFQKHIAKRCCKCSIFQKEAPERANSVYTRSTGEQVSAGL 352

RESULT 8
Q18770 PRELIMINARY; PRT; 352 AA.
AC Q18770;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-DEC-2001 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MACCR5-140A;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "Hiv-1 subtypes, co-receptor usage, and CCR5 polymorphism.4;
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011538; AAB65738.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;

Query Match 72.0%; Score 1368; DB 6; Length 352;
Best Local Similarity 76.1%; Pred. No. 7.7e-110;
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDGA--GACHKFDVKQIGAQLLPPLYSLVYFIFGVGNMVLVLLINCKKLCITDIYL 81
Db 10 YDIDYTSEPCQKINVQIAARLLPPLYSLVYFIFGVGNMVLVLLINCKKLSMTDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISDLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
Db 130 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRRHRAVRVIFTMIVYFLEWT 257
Db 190 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRRHRAVRVIFTMIVYFLEWT 249
QY 258 PYNIVILLNTQFEEFGLSNCESTSDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVILLNTQFEEFGLSNCESTSDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309

Query Match 72.2%; Score 1371; DB 6; Length 352;
Best Local Similarity 75.2%; Pred. No. 4.3e-110;
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

QY 24 FDYDGA--PCHKFDVKQIGAQLLPPLYSLVYFIFGVGNMVLVLLINCKKLCITDIYL 81
Db 10 YDIDYGASEPCQKTDVQKGAHLLPPLYSIVLFGVGNMVLVLLINCKKPSMTDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISDLLFLITLPLWAHSAANWVFGNACKLFTGLYHIGYFGGIFFIILLTIDRYLA 129
QY 142 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
Db 130 IVHAFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRRHRAVRVIFTMIVYFLEWT 257
Db 190 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRRHRAVRVIFTMIVYFLEWT 249
QY 258 PYNIVILLNTQFEEFGLSNCESTSDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVILLNTQFEEFGLSNCESTSDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309
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QY 318 VFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGQEQVSAGL 360

Db 310 VFFOKHIAKRFCKCSIFOGEASERASSVYTRSTGQEIEISVGL 352

RESULT 10
Q9MZ99
ID Q9MZ99 PRELIMINARY; PRT; 352 AA.
AC Q9MZ99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Ateles sp. (spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
OX NCBI_TaxId=9511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2037091; PubMed=1074879;
RA Mumudi S., Bانشad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA Begum K., Galois M.C., Kostecki V., Valente A.J., Murthy K.K.,
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT "Evolution of human and non-human primate CC chemokine receptor 5 gen-
RT and mRNA. Potential roles for haplotype and mRNA diversity, and altered
RT differential haplotype-specific transcriptional activities, and altered
RT transcription factor binding to polymorphic nucleotides in the
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
DR EMBL; AF252555; AAP87985.1; -
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40471 MW; 01E397C2A87DE64D CRC64;
Query Match 71.9%; Score 1367; DB 6; Length 352;
Best Local Similarity 74.9%; Pred. No. 9.4e-110;
Matches 257; Conservative 32; Mismatches 48; Indels 6; Gaps
QY 24 FDYDYG-A-PCHKFDVKIQIGAOILPPIYSIVFTFGVGNMLVLILNCCKKLCLTDIYL 81
:       :       :       :       :       :       :       :       :
DB 10 YDIYDGASEPKRTDVVKMGAGHLLPPIYSWVFEGFVGNMLVLILNCKRPSKMTDIYL 69
:       :       :       :       :       :       :       :       :
QY 82 LNLAISDLLFLITPLWAHSAANEWFNGAMCKLFTGLYHGIFGFIFFILITIDRYLA 141
:       :       :       :       :       :       :       :       :
DB 70 LNLATISDLLFLTVPFWAHVAAGOWDGTMCQFLTGLYFI GFSGIFFILITIDRYLA 129
:       :       :       :       :       :       :       :       :
QY 142 IVHAVFAALKARTVTFGVVTSVITWLVAFAVSVCIIETKCOKEDSVVCGPYPRG--- 197
:       :       :       :       :       :       :       :       :
DB 130 IVHAVFAALKARTVFGVMTSVITWLVAFAVSFCIIETRCNEKRHRRAVRVIFTMIVYLFWT 257
:       :       :       :       :       :       :       :       :
QY 198 WNNFHTLMRNILGLVLPPLLNMVICYSGIKLTLCRCNEKRHRRAVRVIFTMIVYLFWT 249
:       :       :       :       :       :       :       :       :
DB 190 WKNFETLKMWILGLVLPPLVNMVICYSGIKLTLCRCNEKRHRRAVRVIFTMIVYLFWA 249
:       :       :       :       :       :       :       :       :
QY 258 PYNVILLNTFQEFGLSNCESTSQLDAQTVTETLGMTHCCINPIIYAIVGGEKFRYLS 317
:       :       :       :       :       :       :       :       :
DB 250 PYNVILLNTYQEEFGLNCSNSSNRDLQAQVTETLGMTHCCVNPPIIYAIVGGEKFRYLL 309
:       :       :       :       :       :       :       :       :
QY 318 VFFRKHTTKRKCPKYFYETVDGVTSTNTPSPGEOVSAGL 360
:       :       :       :       :       :       :       :       :
DB 310 VFFOKHTAKCECCSFQKEAPERANSVYTRSTGEQEI SVGL 352
:       :       :       :       :       :       :       :       :
RESULT 11
Q95ND1

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ID Q95ND1 PRELIMINARY; PRT; 352 AA;
AC Q95ND1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DR 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Mandrillus sphinx (Mandrill) (Papio sphinx).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Mandrillus.
OX NCBI_TaxID=9561;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177897; AAK43360.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40510 MW; 402D8543DDD3AEDD CRC64;

Query Match 71.9%; Score 1366; DB 6; Length 352;
Best Local Similarity 76.1%; Pred. No. 1.1e-109;
Matches 261; Conservative 30; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKQIGAOQLPLYSLSVIFGFGNMLVLLINCKKLKCLTDIYL 81
DB 10 YDIDYTSPPCKQKINVKQIAHLLPLKSLVIFGFGNMLVLLINCKRLKSMTDIYL 69
QY 82 LNLAISDLLFLTLPLWAHSAANEWFGNACMLTGLYHIGYFGGIFFIILLTDIYLA 141
DB 70 LNLAISDLLFLTLVFWAHYAAQWDFGNIMCQLLTGLYFGGIFFIILLTDIYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG 197
DB 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGLHYTCSSHPFYQYOF 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVIFTIMIVYFLWT 257
DB 190 WKNFRTLAIVLGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVIFTIMIVYFLWA 249
QY 258 PYNIVLLNTQEFPGLSNCESTSLDQATQVTELTGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTQEFPGLSNCESTSLDQATQVTELTGMTHCCINPIIYAFVGEKFRNYLL 309
QY 318 VFERKHITKRCCKCPVEYRETVDGVTSTNTPSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQEISVGL 352

RESULT 12
Q95NC0 PRELIMINARY; PRT; 352 AA.
AC Q95NC0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DR 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates moloch (silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
phylogeny."

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RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177899; AAK43382.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 71.9%; Score 1366; DB 6; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.1e-109;
Matches 260; Conservative 30; Mismatches 47; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKQIGAOQLPLYSLSVIFGFGNMLVLLINCKKLKCLTDIYL 81
DB 10 YDIDYTSPPCKQKINVKQIAARLLPPLYSLSVIFGFGNMLVLLINCKRLKSMTDIYL 69
QY 82 LNLAISDLLFLTLPLWAHSAANEWFGNACMLTGLYHIGYFGGIFFIILLTDIYLA 141
DB 70 LNLAISDLLFLTLVFWAHYAAQWDFGNIMCQLLTGLYFGGIFFIILLTDIYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG 197
DB 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGLHYTCSSHPFYQYOF 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVIFTIMIVYFLWT 257
DB 190 WKNFRTLAIVLGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVIFTIMIVYFLWA 249
QY 258 PYNIVLLNTQEFPGLSNCESTSLDQATQVTELTGMTHCCINPIIYAFVGEKFRYLS 317
DB 250 PYNIVLLNTQEFPGLSNCESTSLDQATQVTELTGMTHCCINPIIYAFVGEKFRNYLL 309
QY 318 VFERKHITKRCCKCPVEYRETVDGVTSTNTPSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQEISVGL 352

RESULT 13
Q9XS99 PRELIMINARY; PRT; 352 AA.
AC Q9XS99;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GORILLACCR;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR EMBL; AF105291; AAD20560.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 71.8%; Score 1365; DB 6; Length 352;
Best Local Similarity 75.8%; Pred. No. 1.4e-109;
Matches 260; Conservative 31; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKQIGAOQLPLYSLSVIFGFGNMLVLLINCKKLKCLTDIYL 81

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Db 10 YDIYTSPOCKNTWKQTAARLLPPLYSLVIFGFGNMLVILILINCKRLKSMTDIYL 69  
QY 82 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
Db 70 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 129  
QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVYCGPYEP---RG 197  
Db 130 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVYCGPYEP---RG 199  
QY 198 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257  
Db 190 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 249  
QY 258 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317  
Db 250 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309  
QY 318 VFERKHTKRCCKOCVPEYRETVDGVTSTNTPTSGEQEVSAGL 360  
Db 310 VFERKHTKRCCKOCVPEYRETVDGVTSTNTPTSGEQEVSAGL 352

## RESULT 14

Q95NC5 PRELIMINARY; PRT; 352 AA.  
AC Q95NC5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.  
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=9590;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
phylogeny."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF177884; AAK43367.1;  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40508 MW; P4F64B3AD5AF658A CRC64;

Query Match 71.8%; Score 1365; DB 6; Length 352;  
Best Local Similarity 75.8%; Pred. No. 1.4e-109;  
Matches 260; Conservative 30; Mismatches 47; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVQIGAGQLPPLYSLVIFGFGNMLVILILINCKRLKSMTDIYL 81  
Db 10 YDIYTSPOCKNTWKQTAARLLPPLYSLVIFGFGNMLVILILINCKRLKSMTDIYL 69  
QY 82 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
Db 70 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 129  
QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVYCGPYEP---RG 197  
Db 130 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVYCGPYEP---RG 199  
QY 198 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257  
Db 190 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 249  
QY 258 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317  
Db 250 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309

Db 250 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309  
QY 318 VFERKHTKRCCKOCVPEYRETVDGVTSTNTPTSGEQEVSAGL 360  
Db 310 VFERKHTKRCCKOCVPEYRETVDGVTSTNTPTSGEQEVSAGL 352  
RESULT 15  
Q95ND2 PRELIMINARY; PRT; 352 AA.  
AC Q95ND2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.  
OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Mandrillus.  
OX NCBI\_TaxID=9568;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
phylogeny."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF177876; AAK43359.1;  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40543 MW; 4C0CF4A2B8E5EFAF CRC64;

Query Match 71.8%; Score 1364; DB 6; Length 352;  
Best Local Similarity 75.8%; Pred. No. 1.7e-109;  
Matches 260; Conservative 32; Mismatches 45; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVQIGAGQLPPLYSLVIFGFGNMLVILILINCKRLKSMTDIYL 81  
Db 10 YDIYTSPOCKNTWKQTAARLLPPLYSLVIFGFGNMLVILILINCKRLKSMTDIYL 69  
QY 82 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141  
Db 70 LNLAISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 129  
QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVYCGPYEP---RG 197  
Db 130 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVYCGPYEP---RG 189  
QY 198 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257  
Db 190 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 249  
QY 258 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 317  
Db 250 PYNIVILLNTQEFGLNCSSTOLDQATQVETLGMTHCCINPIIYAFVGEKFRYLS 309  
QY 318 VFERKHTKRCCKOCVPEYRETVDGVTSTNTPTSGEQEVSAGL 360  
Db 310 VFERKHTKRCCKOCVPEYRETVDGVTSTNTPTSGEQEVSAGL 352

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Job time : 56.4414 secs

